

CAGCCCTCAT CTCCGCCGGC GAGTAGGGCC AGGTGTTGGG AGCTCCCACG TGGGACAAGG 60
 TGGTGTCTTC GGCGCAG 77

atg ggt ttc aac cag cag gct ctc ctg gag cag ctc agc cag gat gag 125
 Met Gly Phe Asn Leu Gln Ala Leu Leu Glu Gln Leu Ser Gln Asp Glu
 1 5 10 15

ttg agc aag ttc aag tat ctg atc acg acc ttc tcc ccg gca cac gag 173
 Leu Ser Lys Phe Lys Tyr Leu Ile Thr Thr Phe Ser Pro Ala His Glu
 20 25 30

ctc cag aag atc ccc cac aag gag gta gac aag gct gat ggg aag caa 221
 Leu Gln Lys Ile Pro His Lys Glu Val Asp Lys Ala Asp Gly Lys Gln
 35 40 45

ctg gta gaa atc ctc acc acc cat tgt gac agc tac tgg gtg gag atg 269
 Leu Val Glu Ile Leu Thr Thr His Cys Asp Ser Tyr Trp Val Glu Met
 50 55 60

gcg agc ctc cag gtc ttt gaa aag atg cac cga atg gat ctg tct gag 317
 Ala Ser Leu Gln Val Phe Glu Lys Met His Arg Met Asp Leu Ser Glu
 65 70 75 80

aga gca aag gat gaa gtc aga gaa gca gct ttg aaa tcc ttt aat aaa 365
 Arg Ala Lys Asp Glu Val Arg Glu Ala Ala Leu Lys Ser Phe Asn Lys
 85 90 95

agg aag cct cta tca tta ggg ata aca cgg aaa gaa cga cca cct cta 413
 Arg Lys Pro Leu Ser Leu Gly Ile Thr Arg Lys Glu Arg Pro Pro Leu
 100 105 110

gac gtg gac gaa atg ctg gag cgc ttc aaa aca gaa gca caa gac aaa 461
 Asp Val Asp Glu Met Leu Glu Arg Phe Lys Thr Glu Ala Gln Asp Lys
 115 120 125

gac aat agg tgc agg tat ata ttg aag acg aag ttc cgg gag atg tgg 509
 Asp Asn Arg Cys Arg Tyr Ile Leu Lys Thr Lys Phe Arg Glu Met Trp
 130 135 140

aag agc tgg cct gga gat agc aaa gag gtc cag gtt atg gct gag aga 557
 Lys Ser Trp Pro Gly Asp Ser Lys Glu Val Gln Val Met Ala Glu Arg
 145 150 155 160

tac aag atg ctg atc cca ttt agc aac ccc agg gtg ctt ccc ggg ccc 605
 Tyr Lys Met Leu Ile Pro Phe Ser Asn Pro Arg Val Leu Pro Gly Pro
 165 170 175

ttc tca tac acg gtg gtg ctg tat ggt cct gca ggc ctt ggg aaa acc 653
 Phe Ser Tyr Thr Val Val Leu Tyr Gly Pro Ala Gly Leu Gly Lys Thr
 180 185 190

acg ctg gcc cag aaa cta atg cta gac tgg gca gag gac aac ctc atc 701
 Thr Leu Ala Gln Lys Leu Met Leu Asp Trp Ala Glu Asp Asn Leu Ile
 195 200 205

FIG. 1A

cac aaa ttc aaa tat gcg ttc tac ctc agc tgc agg gag ctc agc cgc His Lys Phe Lys Tyr Ala Phe Tyr Leu Ser Cys Arg Glu Leu Ser Arg 210 215 220	749
ctg ggc ccg tgc agt ttt gca gag ctg gtc ttc agg gac tgg cct gaa Leu Gly Pro Cys Ser Phe Ala Glu Leu Val Phe Arg Asp Trp Pro Glu 225 230 235 240	797
ttg cag gat gac att cca cac atc cta gcc caa gca cgg aaa atc ttg Leu Gln Asp Asp Ile Pro His Ile Leu Ala Gln Ala Arg Lys Ile Leu 245 250 255	845
ttc gtg att gac ggc ttt gat gag ctg gga gcc gca cct ggg gcg ctg Phe Val Ile Asp Gly Phe Asp Glu Leu Gly Ala Ala Pro Gly Ala Leu 260 265 270	893
atc gag gac atc tgc ggg gac tgg gag aag aag aag ccg gtg ccc gtc Ile Glu Asp Ile Cys Gly Asp Trp Glu Lys Lys Lys Pro Val Pro Val 275 280 285	941
ctc ctg ggg agt ttg ctg aac agg gtg atg tta ccc aag gcc gcc ctg Leu Leu Gly Ser Leu Leu Asn Arg Val Met Leu Pro Lys Ala Ala Leu 290 295 300	989
ctg gtc acc acg cgg ccc agg gcc ctg agg gac ctc cgg atc ctg gcg Leu Val Thr Thr Arg Pro Arg Ala Leu Arg Asp Leu Arg Ile Leu Ala 305 310 315 320	1037
gag gag ccg atc tac ata agg gtg gag ggc ttc ctg gag gag gac aag Glu Glu Pro Ile Tyr Ile Arg Val Glu Gly Phe Leu Glu Glu Asp Lys 325 330 335	1085
agg gcc tat ttc ctg aga cac ttt gga gac gag gac caa gcc atg cgt Arg Ala Tyr Phe Leu Arg His Phe Gly Asp Glu Asp Gln Ala Met Arg 340 345 350	1133
gcc ttt gag cta atg agg agc aac gcg gcc ctg ttc cag ctg ggc tgc Ala Phe Glu Leu Met Arg Ser Asn Ala Ala Leu Phe Gln Leu Gly Ser 355 360 365	1181
gcc ccc gcg gtg tgc tgg atc gtg tgc acg act ctg aag ctg cag atg Ala Pro Ala Val Cys Trp Ile Val Cys Thr Thr Leu Lys Leu Gln Met 370 375 380	1229
gag aag ggg gag gac ccg gtc ccc acc tgc ctc acc cgc acg ggg ctg Glu Lys Gly Glu Asp Pro Val Pro Thr Cys Leu Thr Arg Thr Gly Leu 385 390 395 400	1277
ttc ctg cgt ttc ctc tgc agc cgg ttc ccg cag ggc gca cag ctg cgg Phe Leu Arg Phe Leu Cys Ser Arg Phe Pro Gln Gly Ala Gln Leu Arg 405 410 415	1325
ggc gcg ctg cgg acg ctg agc ctc ctg gcc gcg cag ggc ctg tgg gcg Gly Ala Leu Arg Thr Leu Ser Leu Leu Ala Ala Gln Gly Leu Trp Ala 420 425 430	1373

FIG. 1B

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NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN FAMILY AND USES THEREOF

[REDACTED]

FIG. 1C

1

[illegible]

FIG. 1D

NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

ata act agc gat ggc tgc tgc gat ctc aca aag ctt ctc caa gaa aaa	2765
Ile Thr Ser Asp Gly Cys Cys Asp Leu Thr Lys Leu Leu Gln Glu Lys	
885 890 895	
tca agc ctg ttg tgt ttg gat ctg ggg ctg aat cac ata gga gtt aag	2813
Ser Ser Leu Leu Cys Leu Asp Leu Gly Leu Asn His Ile Gly Val Lys	
900 905 910	
gga atg aag ttc ctg tgt gag gct ttg agg aaa cca ctg tgc aac ttg	2861
Gly Met Lys Phe Leu Cys Glu Ala Leu Arg Lys Pro Leu Cys Asn Leu	
915 920 925	
aga tgt ctg tgg ttg tgg gga tgt tcc atc cct ccg ttc agt tgt gaa	2909
Arg Cys Leu Trp Leu Trp Gly Cys Ser Ile Pro Pro Phe Ser Cys Glu	
930 935 940	
gac ctc tgc tct gcc ctc agc aac cag agc ctc gtc act ctg gac ctg	2957
Asp Leu Cys Ser Ala Leu Ser Asn Gln Ser Leu Val Thr Leu Asp Leu	
945 950 955 960	
ggt cag aat ccc ttg ggg tct agt gga gtg aag atg ctg ttt gaa acc	3005
Gly Gln Asn Pro Leu Gly Ser Ser Gly Val Lys Met Leu Phe Glu Thr	
965 970 975	
ttg aca tgt tcc agt ggc acc ctc cgg aca ctc agg ttg aaa atc gat	3053
Leu Thr Cys Ser Ser Gly Thr Leu Arg Thr Leu Arg Leu Lys Ile Asp	
980 985 990	
gac ttt aat gat gaa ctc aat aag ctg ctg gaa gaa ata gaa gaa aaa	3101
Asp Phe Asn Asp Glu Leu Asn Lys Leu Leu Glu Glu Ile Glu Glu Lys	
995 1000 1005	
aac cca caa ctg att att gat act gag aaa cat cat ccc tgg gca gaa	3149
Asn Pro Gln Leu Ile Ile Asp Thr Glu Lys His His Pro Trp Ala Glu	
1010 1015 1020	
agg cct tct tct cat gac ttc atg atc	3176
Arg Pro Ser Ser His Asp Phe Met Ile	
1025 1030	
TGAATCCCCC CGAGTCATTC ATTCTCCATG AAGTCATCGA TTTTCCAGGT GTTGGTGAAC	3236
TGCCTGTGAC TCCTCTCCTC CCCGGCCCCCT ACCCCTCAGG GATAATGAGT TCATTGCTGG	3296
GCTAGATGTT TTAGCCATGA TTCTGCCTCT GTTTTATACC TGCACACATC CTTATCTTTG	3356
TTACATATGA AATATCTGTA TCACGGGTAT ATTGAGAGAA ATAAAGGTGA GAGCATTAC	3416
AAAAAAAAAA AAAAAA	3431

FIG. 1E

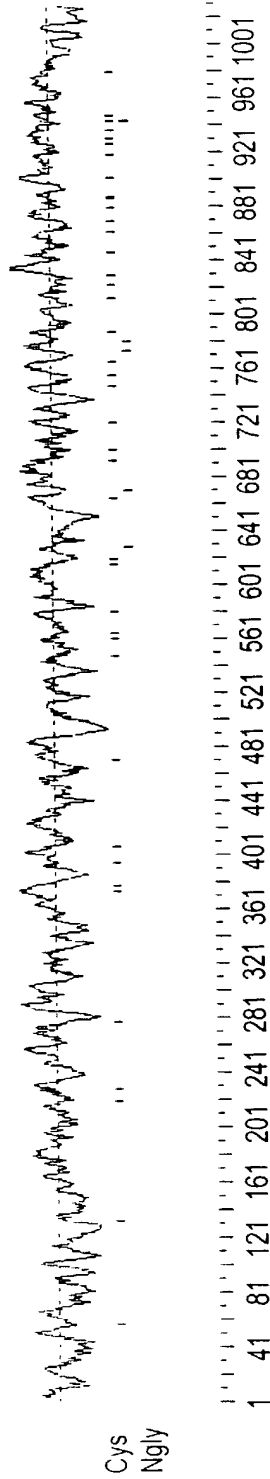
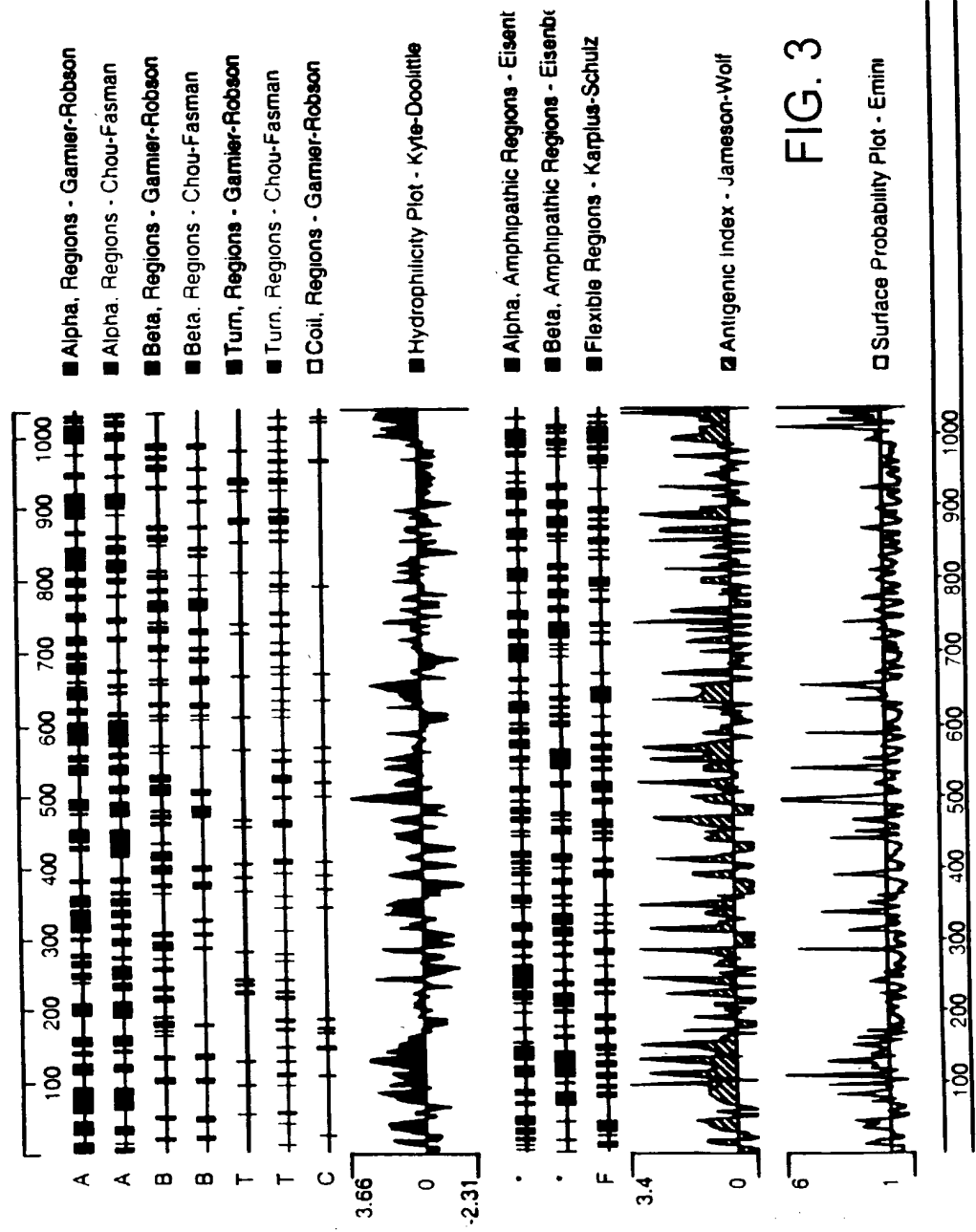


FIG. 2



ccacgcgtcc gccacgcgt ccgggcatct ggggaaacct ttcttccatg gctcaggaca	60
cactcctgga tcgagccaac aggagaactt tctgtgtgga ccgaagccta aggaccctga	120
aaacagctgc agatgaag atg gca agc acc cgc tgc aag ctg gcc agg tac	171
Met Ala Ser Thr Arg Cys Lys Leu Ala Arg Tyr	
1 5 10	
ctg gag gac ctg gag gat gtg gac ttg aag aaa ttt aag atg cac tta	219
Leu Glu Asp Leu Glu Asp Val Asp Leu Lys Lys Phe Lys Met His Leu	
15 20 25	
gag gac tat cct ccc cag aag ggc tgc atc ccc ctc ccg agg ggt cag	267
Glu Asp Tyr Pro Pro Gln Lys Gly Cys Ile Pro Leu Pro Arg Gly Gln	
30 35 40	
aca gag aag gca gac cat gtg gat cta gcc acg cta atg atc gac ttc	315
Thr Glu Lys Ala Asp His Val Asp Leu Ala Thr Leu Met Ile Asp Phe	
45 50 55	
aat ggg gag gag aag gcg tgg gcc atg gcc gtg tgg atc ttc gct gcg	363
Asn Gly Glu Glu Lys Ala Trp Ala Met Ala Val Trp Ile Phe Ala Ala	
60 65 70 75	
atc aac agg aga gac ctt tat gag aaa gca aaa aga gat gag ccg aag	411
Ile Asn Arg Arg Asp Leu Tyr Glu Lys Ala Lys Arg Asp Glu Pro Lys	
80 85 90	
tgg ggt tca gat aat gca cgt gtt tcg aat ccc act gtg ata tgc cag	459
Trp Gly Ser Asp Asn Ala Arg Val Ser Asn Pro Thr Val Ile Cys Gln	
95 100 105	
gaa gac agc att gaa gag gag tgg atg ggt tta ctg gag tac ctt tcg	507
Glu Asp Ser Ile Glu Glu Glu Trp Met Gly Leu Leu Glu Tyr Leu Ser	
110 115 120	
aga atc tct att tgt aaa atg aag aaa gat tac cgt aag aag tac aga	555
Arg Ile Ser Ile Cys Lys Met Lys Lys Asp Tyr Arg Lys Lys Tyr Arg	
125 130 135	
aag tac gtg aga agc aga ttc cag tgc att gaa gac agg aat gcc cgt	603
Lys Tyr Val Arg Ser Arg Phe Gln Cys Ile Glu Asp Arg Asn Ala Arg	
140 145 150 155	
ctg ggt gag agt gtg agc ctc aac aaa cgc tac aca cga ctg cgt ctc	651
Leu Gly Glu Ser Val Ser Leu Asn Lys Arg Tyr Thr Arg Leu Arg Leu	
160 165 170	
atc aag gag cac cgg agc cag cag gag agg gag cag gag ctt ctg gcc	699
Ile Lys Glu His Arg Ser Gln Gln Glu Arg Glu Gln Glu Leu Leu Ala	
175 180 185	
atc ggc aag acc aag acg tgt gag agc ccc gtg agt ccc att aag atg	747
Ile Gly Lys Thr Lys Thr Cys Glu Ser Pro Val Ser Pro Ile Lys Met	
190 195 200	
gag ttg ctg ttt gac ccc gat gat gag cat tct gag cct gtg cac acc	795
Glu Leu Leu Phe Asp Pro Asp Asp Glu His Ser Glu Pro Val His Thr	
205 210 215	

FIG. 4A

NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

gtg gtg ttc cag ggg gcg gca ggg att ggg aaa aca atc ctg gcc agg	843
Val Val Phe Gln Gly Ala Ala Gly Ile Gly Lys Thr Ile Leu Ala Arg	
220 225 230 235	
aag atg atg ttg gac tgg gca tgg ggg aca ctc tac caa gac agg ttt	891
Lys Met Met Leu Asp Trp Ala Ser Gly Thr Leu Tyr Gln Asp Arg Phe	
240 245 250	
gac tat ctg ttc tat atc cac tgt cgg gag gtg agc ctt gtg aca cag	939
Asp Tyr Leu Phe Tyr Ile His Cys Arg Glu Val Ser Leu Val Thr Gln	
255 260 265	
agg agc ctg ggg gac ctg atc atg agc tgc tgc ccc gac cca aac cca	987
Arg Ser Leu Gly Asp Leu Ile Met Ser Cys Cys Pro Asp Pro Asn Pro	
270 275 280	
ccc atc cac aag atc gtg aga aaa ccc tcc aga atc ctc ttc ctc atg	1035
Pro Ile His Lys Ile Val Arg Lys Pro Ser Arg Ile Leu Phe Leu Met	
285 290 295	
gac ggc ttc gat gag ctg caa ggt gcc ttt gac gag cac ata gga ccg	1083
Asp Gly Phe Asp Glu Leu Gln Gly Ala Phe Asp Glu His Ile Gly Pro	
300 305 310 315	
ctc tgc act gac tgg cag aag gcc gag cgg gga gac att ctc ctg agc	1131
Leu Cys Thr Asp Trp Gln Lys Ala Glu Arg Gly Asp Ile Leu Leu Ser	
320 325 330	
agc ctc atc aga aag aag ctg ctt ccc gag gcc tct ctg ctc atc acc	1179
Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Ala Ser Leu Leu Ile Thr	
335 340 345	
acg aga cct gtg gcc ctg gag aaa ctg cag cac ttg ctg gac cat cct	1227
Thr Arg Pro Val Ala Leu Glu Lys Leu Gln His Leu Leu Asp His Pro	
350 355 360	
cgg cat gtg gag atc ctg ggt ttc tcc gag gcc aaa agg aaa gag tac	1275
Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala Lys Arg Lys Glu Tyr	
365 370 375	
ttc ttc aag tac ttc tct gat gag gcc caa gcc agg gca gcc ttc agt	1323
Phe Phe Lys Tyr Phe Ser Asp Glu Ala Gln Ala Arg Ala Ala Phe Ser	
380 385 390 395	
ctg att cag gag aac gag gtc ctc ttc acc atg tgc ttc atc ccc ctg	1371
Leu Ile Gln Glu Asn Glu Val Leu Phe Thr Met Cys Phe Ile Pro Leu	
400 405 410	
gtc tgc tgg atc gtg tgc act gga ctg aaa cag cag atg gag agt ggc	1419
Val Cys Trp Ile Val Cys Thr Gly Leu Lys Gln Gln Met Glu Ser Gly	
415 420 425	
aag agc ctt gcc cag aca tct aag acc acc acc gcg gtg tac gtc ttc	1467
Lys Ser Leu Ala Gln Thr Ser Lys Thr Thr Thr Ala Val Tyr Val Phe	
430 435 440	

FIG. 4B

ttc ctt tcc agt ttg ctg cag ccc cgg gga ggg agc cag gag cac ggc	1515
Phe Leu Ser Ser Leu Leu Gln Pro Arg Gly Gly Ser Gln Glu His Gly	
445 450 455	
ctc tgc gcc cac ctc tgg ggg ctc tgc tct ttg gct gca gat gga atc	1563
Leu Cys Ala His Leu Trp Gly Leu Cys Ser Leu Ala Ala Asp Gly Ile	
460 465 470 475	
tgg aac cag aaa atc ctg ttt gag gag tcc gac ctc agg aat cat gga	1611
Trp Asn Gln Lys Ile Leu Phe Glu Glu Ser Asp Leu Arg Asn His Gly	
480 485 490	
ctg cag aag gcg gat gtg tct gct ttc ctg agg atg aac ctg ttc caa	1659
Leu Gln Lys Ala Asp Val Ser Ala Phe Leu Arg Met Asn Leu Phe Gln	
495 500 505	
aag gaa gtg gac tgc gag aag ttc tac agc ttc atc cac atg act ttc	1707
Lys Glu Val Asp Cys Glu Lys Phe Tyr Ser Phe Ile His Met Thr Phe	
510 515 520	
cag gag ttc ttt gcc gcc atg tac tac ctg ctg gaa gag gaa aag gaa	1755
Gln Glu Phe Phe Ala Ala Met Tyr Tyr Leu Leu Glu Glu Lys Glu	
525 530 535	
gga agg acg aac gtt cca ggg agt cgt ttg aag ctt ccc agc cga gac	1803
Gly Arg Thr Asn Val Pro Gly Ser Arg Leu Lys Leu Pro Ser Arg Asp	
540 545 550 555	
gtg aca gtc ctt ctg gaa aac tat ggc aaa ttc gaa aag ggg tat ttg	1851
Val Thr Val Leu Leu Glu Asn Tyr Gly Lys Phe Glu Lys Gly Tyr Leu	
560 565 570	
att ttt gtt gta cgt ttc ctc ttt ggc ctg gta aac cag gag agg acc	1899
Ile Phe Val Val Arg Phe Leu Phe Gly Leu Val Asn Gln Glu Arg Thr	
575 580 585	
tcc tac ttg gag aag aaa tta agt tgc aag atc tct cag caa atc agg	1947
Ser Tyr Leu Glu Lys Lys Leu Ser Cys Lys Ile Ser Gln Gln Ile Arg	
590 595 600	
ctg gag ctg ctg aaa tgg att gaa gtg aaa gcc aaa gct aaa aag ctg	1995
Leu Glu Leu Leu Lys Trp Ile Glu Val Lys Ala Lys Ala Lys Lys Leu	
605 610 615	
cag atc cag ccc agc cag ctg gaa ttg ttc tac tgt ttg tac gag atg	2043
Gln Ile Gln Pro Ser Gln Leu Glu Leu Phe Tyr Cys Leu Tyr Glu Met	
620 625 630 635	
cag gag gag gac ttc gtg caa agg gcc atg gac tat ttc ccc aag att	2091
Gln Glu Glu Asp Phe Val Gln Arg Ala Met Asp Tyr Phe Pro Lys Ile	
640 645 650	
gag atc aat ctc tcc acc aga atg gac cac atg gtt tct tcc ttt tgc	2139
Glu Ile Asn Leu Ser Thr Arg Met Asp His Met Val Ser Ser Phe Cys	
655 660 665	

FIG. 4C

NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN FAMILY AND USES THEREOF

FIG. 4D

tct ggc ctt acg tca gtc tgt tgt tca gct ttg tcc tcg gta ctc agc	2859
Ser Gly Leu Thr Ser Val Cys Cys Ser Ala Leu Ser Ser Val Leu Ser	
895 900 905	
act aat cag aat ctc acg cac ctt tac ctg cga ggc aac act ctc gga	2907
Thr Asn Gln Asn Leu Thr His Leu Tyr Leu Arg Gly Asn Thr Leu Gly	
910 915 920	
gac aag ggg atc aaa cta ctc tgt gag gga ctc ttg cac ccc gac tgc	2955
Asp Lys Gly Ile Lys Leu Leu Cys Glu Gly Leu Leu His Pro Asp Cys	
925 930 935	
aag ctt cag gtg ttg gaa tta gac aac tgc aac ctc acg tca cac tgc	3003
Lys Leu Gln Val Leu Glu Leu Asp Asn Cys Asn Leu Thr Ser His Cys	
940 945 950 955	
tgc tgg gat ctt tcc aca ctt ctg acc tcc agc cag agc ctg cga aag	3051
Cys Trp Asp Leu Ser Thr Leu Leu Thr Ser Ser Gln Ser Leu Arg Lys	
960 965 970	
ctg agc ctg ggc aac aat gac ctg ggc gac ctg ggg gtc atg atg ttc	3099
Leu Ser Leu Gly Asn Asn Asp Leu Gly Asp Leu Gly Val Met Met Phe	
975 980 985	
tgt gaa gtg ctg aaa cag cag agc tgc ctc ctg cag aac ctg ggg ttg	3147
Cys Glu Val Leu Lys Gln Gln Ser Cys Leu Leu Gln Asn Leu Gly Leu	
990 995 1000	
tct gaa atg tat ttc aat tat gag aca aaa agt gcg tta gaa aca ctt	3195
Ser Glu Met Tyr Phe Asn Tyr Glu Thr Lys Ser Ala Leu Glu Thr Leu	
1005 1010 1015	
caa gaa gaa aag cct gag ctg acc gtc gtc ttt gag cct tct tgg tag	3243
Gln Glu Glu Lys Pro Glu Leu Thr Val Val Phe Glu Pro Ser Trp *	
1020 1025 1030	
gagtggaaac ggggctgcc aacgccagt ttctccggc cctccagctg ggggccctca	3303
ggtggagaga gctgcgatcc atccaggcca agaccacagc tctgtgatcc ttccggtgga	3363
gtgtcggaga agagagcttg ccgacgatgc ctctctgtgc agagcttgga catctccttt	3423
acgccagggt gaggaagaca ccaggacaat gacagcatcg ggtgttggtc tcatcacagc	3483
gcctcagtta gaggatgttc ctcttggtga cctcatgtaa ttagctcatt caataaagca	3543
ctttctttat ttttctcttc tctgtctaac tttctttttc ctatcttttt ttcttctttg	3603
ttctgtttac ttttgctcat atcatcatc ccgctaact tctattaact gaccataaca	3663
cagaactagt tgactatata ttatgttgaa attttatggc agctatttat ttatttaaat	3723
tttttgtaat agttttgttt tctaataaga aaaatccatg ctttttgtag ctgggtgaaa	3783
attcaggaat atgtaaaact ttttggtatt taattaaatt gattcctttt cttaatttta	3843
aaaaaaaaa aaaa	3857

FIG. 4E

Patent No.: 07334-341001
 Applicant(s): John Bertin et al.
 NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
 FAMILY AND USES THEREOF

13 of 30

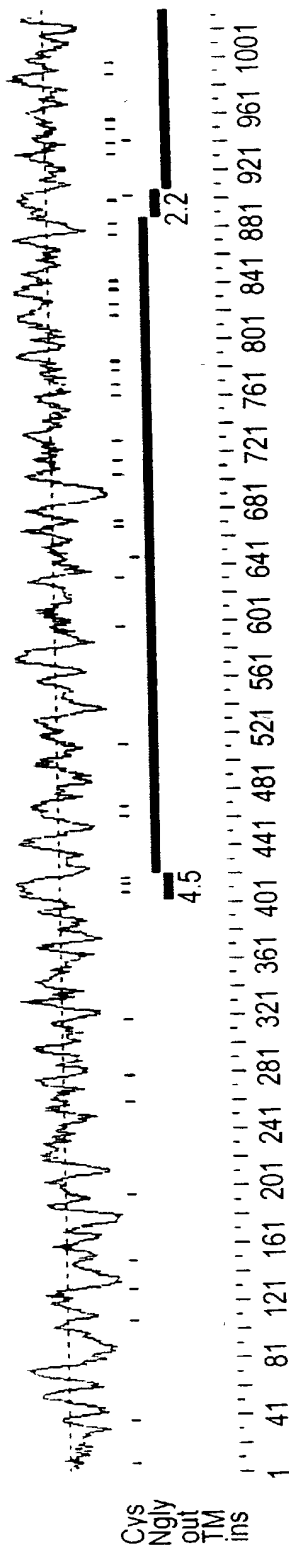
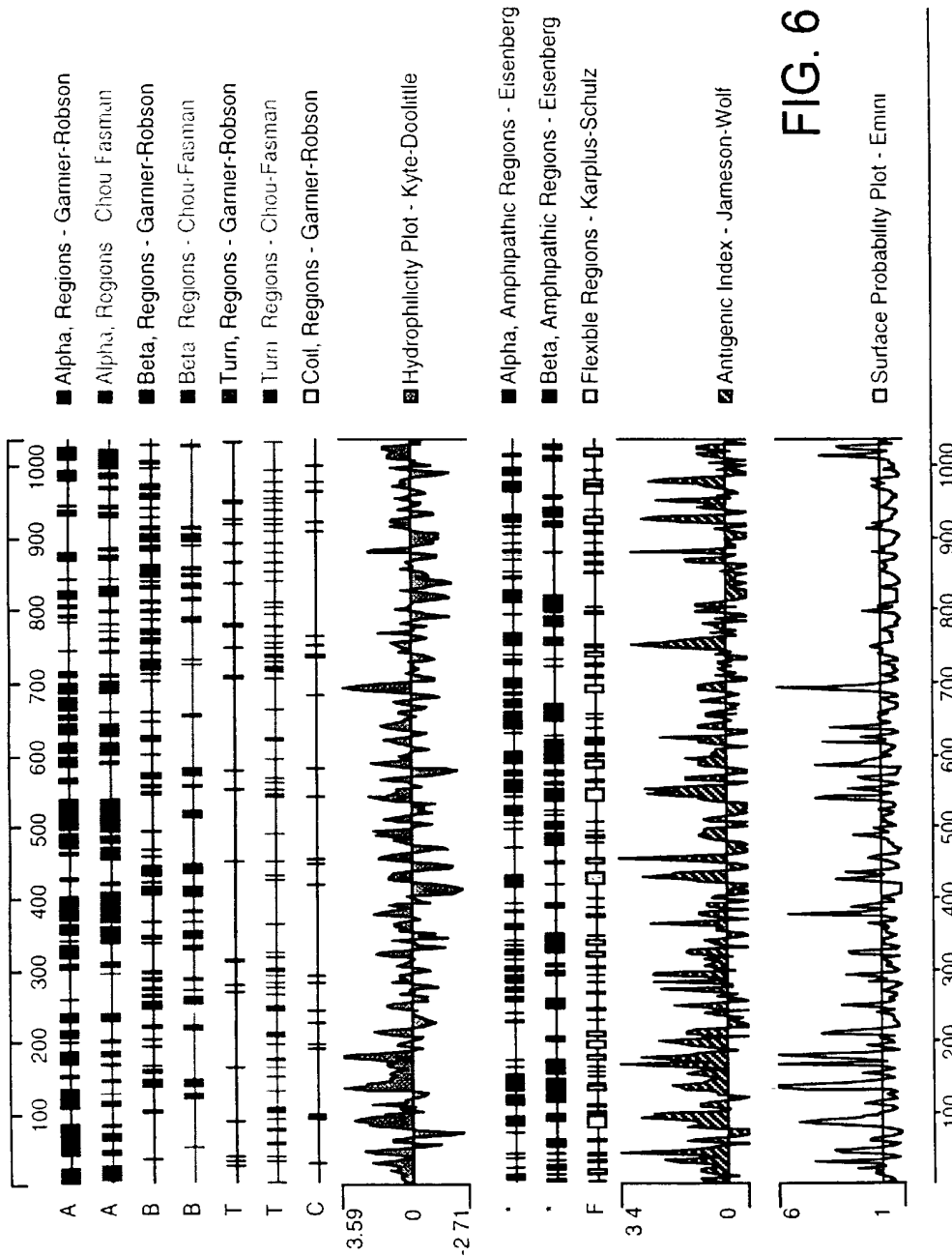


FIG. 5

NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF



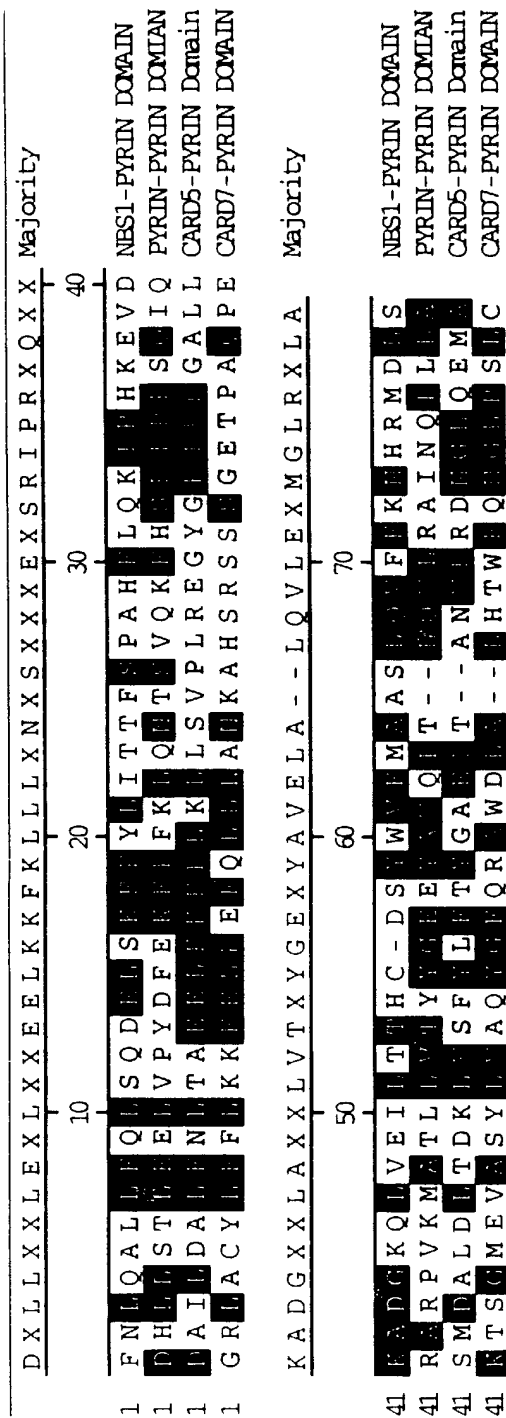


FIG. 7

LRR_RI_2: domain 1 of 8, from 726 to 752: score 0.1, E =
 *-->npsLreLdLsnNklgdeGaralaealks<--
 *** L L++N+ d+ aL+e+L++
 NBS1 726 HKTVTYLTQGNQD-QDDMFALCEVLRH 752

FIG. 8A

LRR_RI_2: domain 2 of 8, from 782 to 809: score 20.8, E = 0.031
 *-->npsLreLdLsnNklgdeGaralaealks<--
 n+sL +Ls+N l deGa+ L +L++
 NBS1 782 NQSLTCVNLSDNELDEGAKLLYTTLRH 809

FIG. 8B

LRR_RI_2: domain 3 of 8, from 811 to 838: score 21.9, E = 0.016
 *-->npsLreLdLsnNklgdeGaralaealks<--
 ** L++L+L+n++l+++ ++ La++L
 NBS1 811 KCFLQRLSLENCHLTEANCKDLAAVLW 838

FIG. 8C

LRR_RI_2: domain 4 of 8, from 839 to 866: score 13.4, E = 0.56

*->npsLrelDlsnNklgdeGaralaealks<--

++ L L L+ N++g G++ L+eL+

NBS1 839 SRELTHLCLAKNPIGNTGKFLCEGLRY 866

FIG. 8D

LRR_RI_2: domain 5 of 8, from 868 to 895: score 17.0, E = 0.17

*->npsLrelDlsnNklgdeGaralaealks<--

++L++L L+n++++ +G+ L ++L++

NBS1 868 ECKLQTLVLWNCDITSDGCCDLTKLLQE 895

FIG. 8E

LRR_RI_2: domain 6 of 8, from 896 to 923: score 22.6, E = 0.0091

*->npsLrelDlsnNklgdeGaralaealks<--

++sL+ LdL+ N++g +G++ L+eal+

NBS1 896 KSSLLCLDLGLNHIGVKGMKFLCEALRK 923

FIG. 8F

LRR_RI_2: domain 7 of 8, from 925 to 952: score 15.8, E = 0.26
->npsLrrelDsnNklgdeGaralaealks<-
+++Lr L+L+++ + + L+al+
NBS1 925 LCNLRCLWLWGCSIPPFSCEDLCSALSN 952

FIG. 8G

LRR_RI_2: domain 8 of 8, from 953 to 979: score 14.0, E = 0.47
->npsLrrelDsnNklgdeGaralaealks<-
+sL +LdL++N+lg +G++ L e+L+
NBS1 953 -QSLVTLDLGQNPLGSSGVKMLFETLTC 979

FIG. 8H

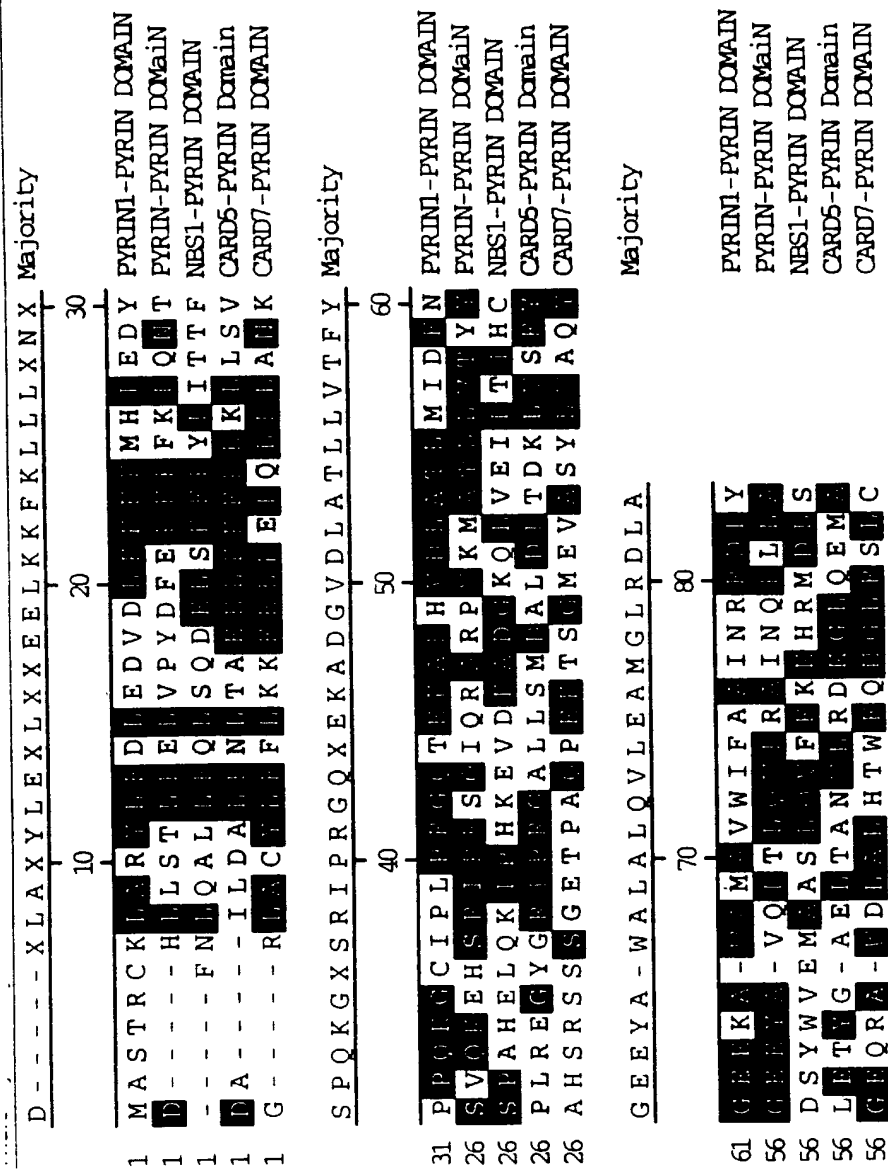


FIG. 9A

NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN FAMILY AND USES THEREOF

PYPAF1	MAS	TR	CK-1	LAR	YLE	D	L	EDVD	LKKFK	MH	L	EDY	P	P	Q	K	G	C	I	P	L	PR	G	O	TE	K	46																			
pyrin	MAK	TPS	DH	LL	ST	LE	E	L	V	P	YDFE	KFK	F	K	L	Q	N	T	S	V	Q	K	E	H	S	R	I	P	47																	
CARD7	MAG	AWGR	L	AC	YLE	F	L	K	K	EELK	E	F	Q	L	L	A	N	K	A	H	S	R	S	S	S	G	E	T	P	47																
ASC	MGR	A	R	-	DA	L	DA	LENLT	A	EELK	F	K	L	L	S	V	P	L	R	E	G	Y	G	R	I	P	R	G	A	L	46															
NBS1	MG	FN	---	L	Q	A	L	LE	Q	L	S	Q	D	E	L	S	K	F	K	Y	L	I	T	T	F	S	P	A	H	E	L	43														
POPI	MGT	K	R	-	E	A	I	L	K	V	L	E	N	L	I	P	E	L	K	K	F	M	K	L	G	T	V	P	L	R	E	G	46													
PYPAF1	AD	H	V	D	L	A	T	L	M	I	D	F	N	G	E	E	K	A	W	A	M	A	V	W	I	F	A	A	I	N	R	R	D	L	Y	E	K	A	K	R	D	--	EP	90		
pyrin	ARP	V	K	M	A	T	L	L	V	T	Y	Y	G	E	E	Y	A	V	Q	L	T	L	Q	V	L	R	A	I	N	Q	R	L	L	A	E	E	L	H	R	A	---	A	90			
CARD7	TS	G	M	E	V	A	S	Y	L	V	A	Q	Y	G	E	Q	R	A	W	D	L	A	L	H	T	W	E	Q	M	G	L	R	S	L	C	A	Q	A	Q	-	E	-	G	A	90	
ASC	MD	A	L	D	L	T	D	K	L	V	S	E	Y	L	E	T	Y	G	A	E	L	T	A	N	V	L	R	D	M	G	L	Q	E	M	A	G	Q	L	Q	A	A	---	T	89		
NBS1	AD	G	K	Q	L	V	E	I	L	T	T	H	C	D	S	Y	W	V	E	M	A	S	L	Q	V	F	E	K	M	H	R	M	D	L	S	E	R	A	K	D	E	V	R	E	A	89
POPI	L	D	I	V	D	L	T	D	K	L	V	A	S	Y	E	D	Y	A	A	E	L	V	V	A	V	L	R	D	M	R	M	L	E	E	A	A	R	L	O	R	A	---	A	89		

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Decoration 'Decoration #2': Shade (with solid black) residues that match the Consensus exactly.

Decoration 'Decoration #3': Box residues that match the Consensus exactly.

FIG. 9B

- LRR: domain 1 of 9, from 740 to 767: score 10.9, E = 25** **FIG. 10A**
 ->nLeeLdLsnN.Lt....slppglfsnLp<-
 +L+eLdLs+N+L +++ + +++++
 pyrin-1 740 SLTELDLSDNsLGdpgmRVLCETLQHPG 767
- LRR: domain 2 of 9, from 769 to 796: score 2.3, E = 4.6e+02** **FIG. 10B**
 ->nLeeLdLsnN.Lt....slppglfsnLp<-
 n+++L+L +++L+++ +++ ++s+ +
 pyrin-1 769 NIRRLWLGRCLShccfDISL-VLSSNQ 796
- LRR: domain 3 of 9, from 797 to 821: score 9.7, E = 39** **FIG. 10C**
 ->nLeeLdLsnN.Lt..slppglfsnLp<-
 +L eLdLs+N L + ++ 1+ +L+
 pyrin-1 797 KLVELDLSdNaLGdfGIRL-LCVGLK 821
- LRR: domain 4 of 9, from 826 to 849: score 4.1, E = 2.5e+02** **FIG. 10D**
 ->nLeeLdLsnN.LtslppglfsnLp<-
 nL++L+L ++ Lts +++
 pyrin-1 826 NLKKLWLVSccLTSACCQDLASVL 849
- LRR: domain 5 of 9, from 854 to 878: score 0.6, E = 8.2e+02** **FIG. 10E**
 ->nLeeLdLsnN.Lt..slppglfsnLp<-
 +L++L++ N L ++++ 1+++ +
 pyrin-1 854 SLTRLYVGENaLGdsGVAI-LCEKAK 878
- LRR: domain 6 of 9, from 883 to 906: score 5.1, E = 1.8e+02** **FIG. 10F**
 ->nLeeLdLsnN.LtslppglfsnLp<-
 nL++L L n +Lts+ +++s+
 pyrin-1 883 NLQKLGLVNSgLTsvccSALSSVL 906
- LRR: domain 7 of 9, from 911 to 935: score 10.2, E = 32** **FIG. 10G**
 ->nLeeLdLsnN.Lt..slppglfsnLp<-
 nL++L+L++N+L ++++ 1+++L
 pyrin-1 911 NLTHLYLRGntLGdkGIKL-LCEGLL 935
- LRR: domain 8 of 9, from 940 to 967: score 5.8, E = 1.4e+02** **FIG. 10H**
 ->nLeeLdLsnN.Lt....slppglfsnLp<-
 +L++L L+n++Lt++ +l+ 1+ + +
 pyrin-1 940 KLQVLELDNCnLTshccwDLST-LLTSSQ 967
- LRR: domain 9 of 9, from 968 to 991: score 8.4, E = 59** **FIG. 10I**
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L+L nN+L +l f+
 pyrin-1 968 SLRKLSLGNNdLGD LGVMMFCEVL 991

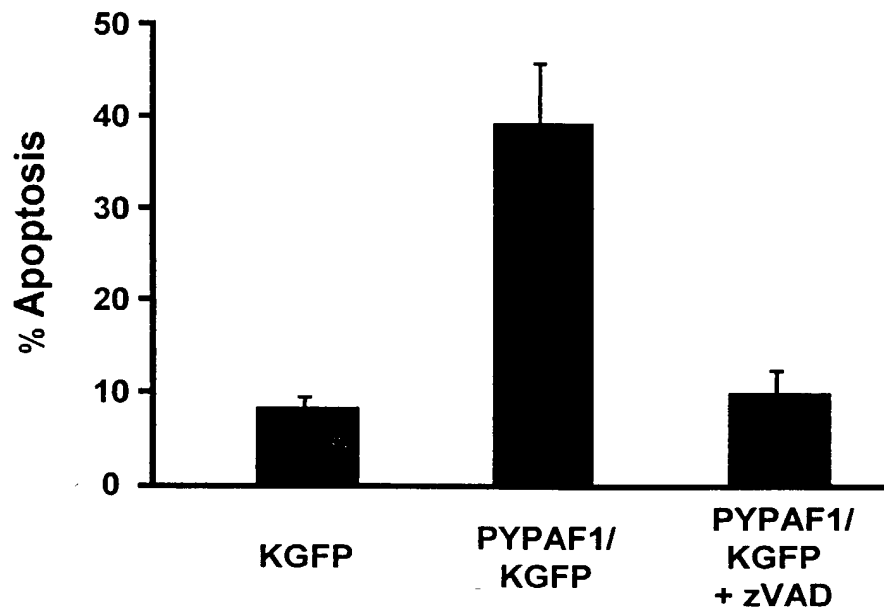


FIG. 11

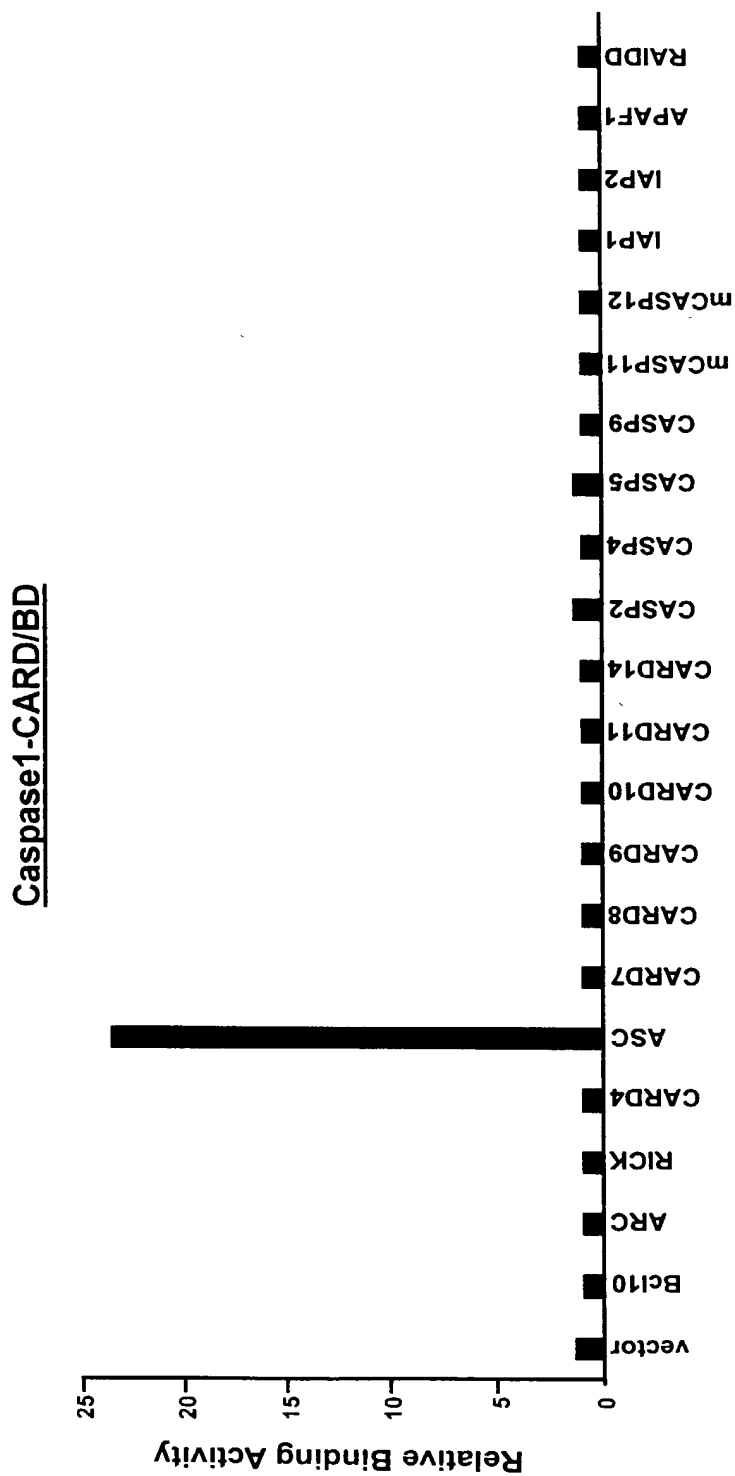


FIG. 12

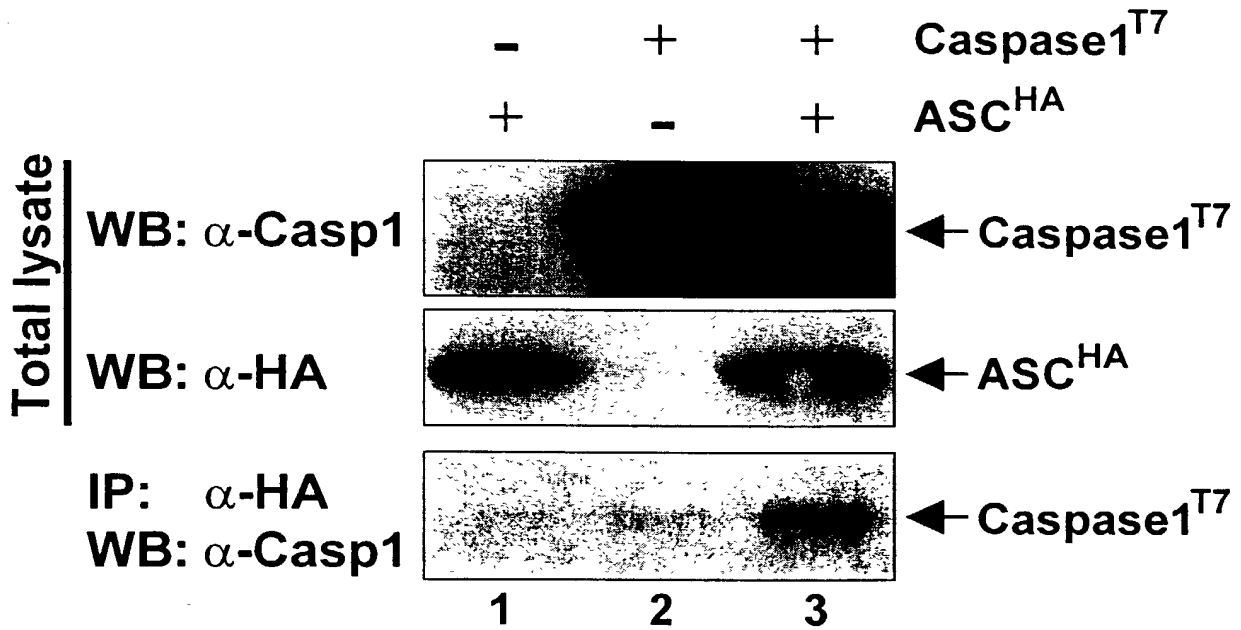


FIG. 13

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NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

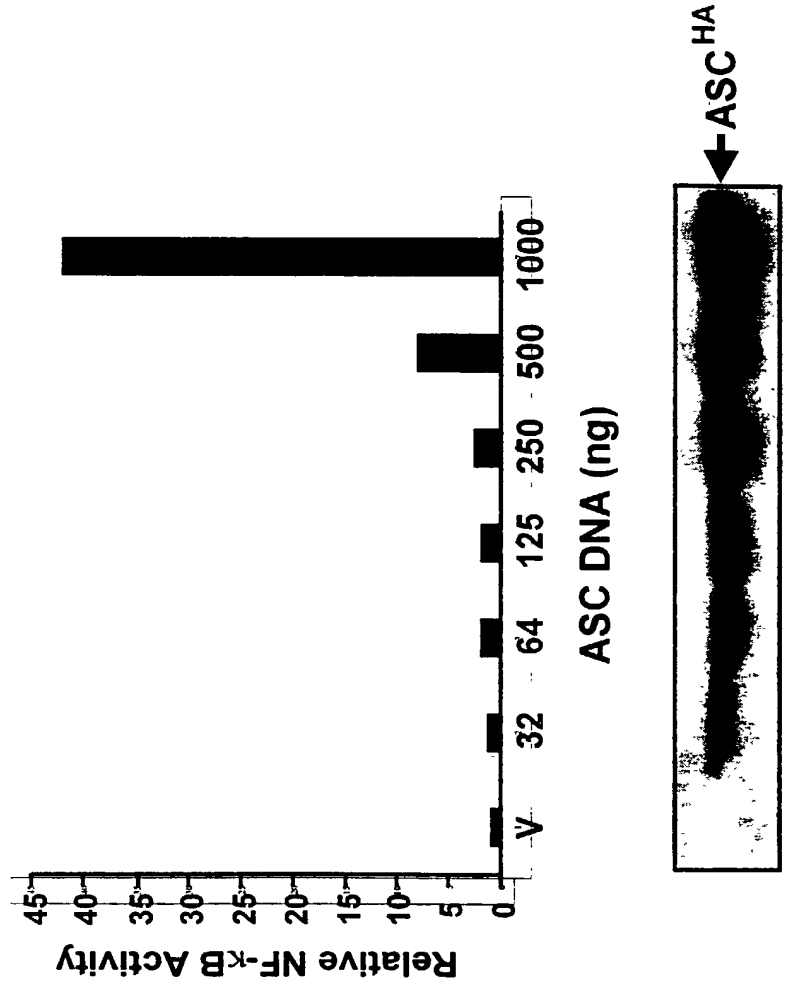


FIG. 14

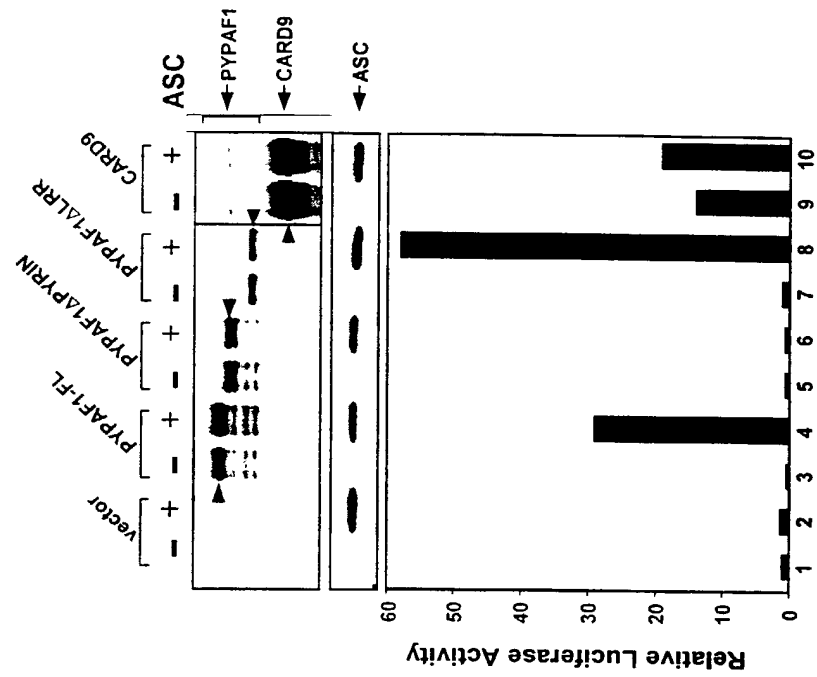


FIG. 15

NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN FAMILY AND USES THEREOF



mPyrin Expression in Normal Mouse Cell Panel



FIG. 17

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NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

Pyrin-1 Expression in ABT Model

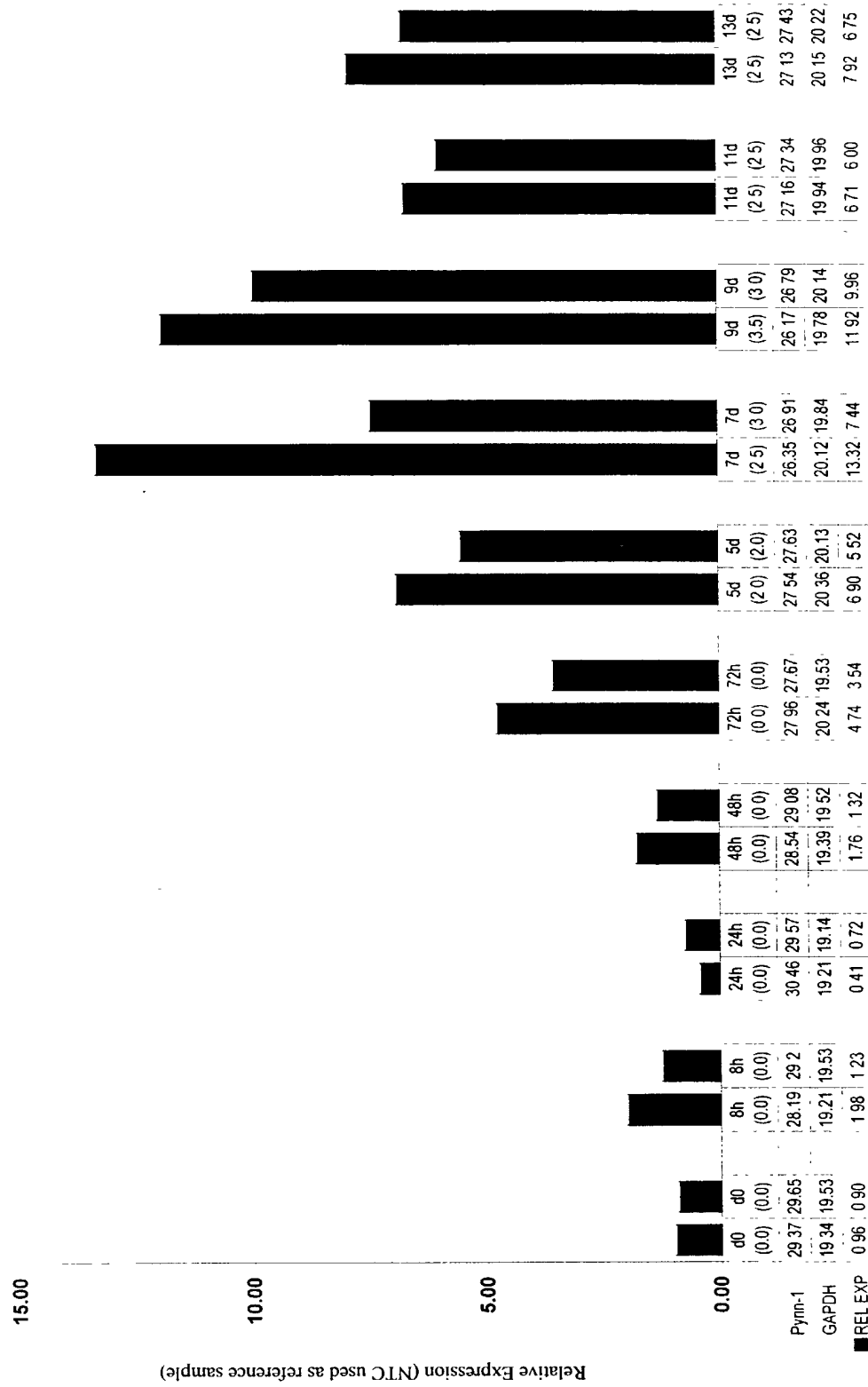


FIG. 18

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NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN
FAMILY AND USES THEREOF

Pyrin-1 Expression in CIA Model

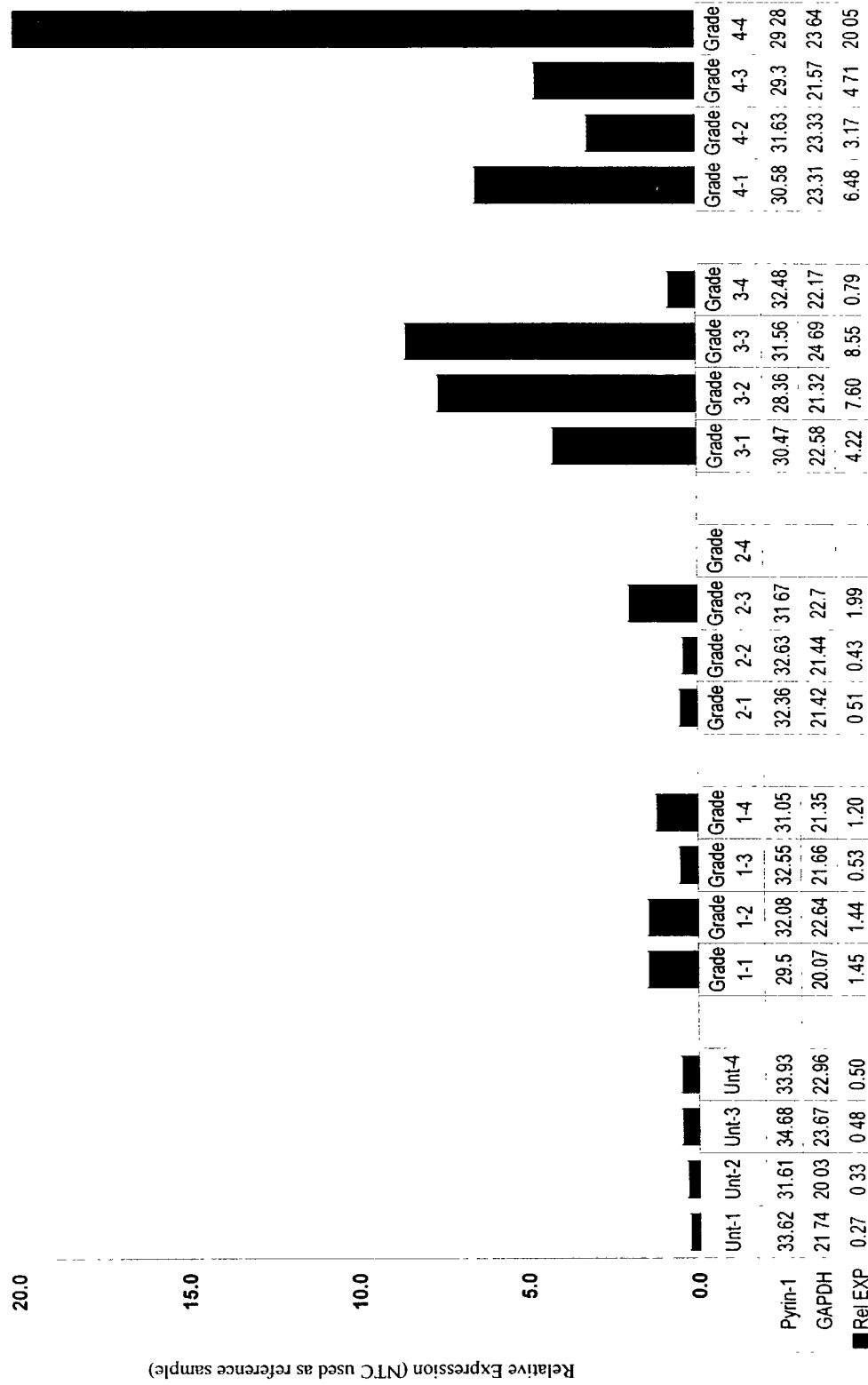


FIG. 19